RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/507,060*

Source: *PCT/10*

Date Processed by STIC: *9/23/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/507,060_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____Wrapped Nucleics
____Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 ____Misaligned Amino
____Numbering
The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 ____Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ____Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____PatentIn 2.0
____"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____Skipped Sequences
____(OLD RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____Skipped Sequences
____(NEW RULES)
Sequence(s) ____ missing. **If intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____Use of n's or Xaa's
____(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____Invalid <213>
____Response
Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ____Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____PatentIn 2.0
____"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____Misuse of n/Xaa "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

RAW SEQUENCE LISTING   DATE: 09/23/2004
PATENT APPLICATION: US/10/507,060   TIME: 11:58:50

Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\09232004\J507060.raw

```
   5 <110> APPLICANT: Baenteli, Rolf
   6         Zenke, Gerhard
   7         Cooke, Nigel Graham
   8         Duthaler, Rudolf
   9         Thoma Gebhard
  10         Von Matt, Anette
  11         Honda, Toshiyuki
  12         Matsuura, Naoko
  13         Nonomura, Kazuhiko
  14         Ohmori, Osamu
  15         Umemura, Ichiro
  16         Hinterding, Klaus
  17         Papageorgiou, Christos
  21 <120> TITLE OF INVENTION: Pyrimidine derivatives
  25 <130> FILE REFERENCE: 4-32366A
C--> 29 <140> CURRENT APPLICATION NUMBER: US/10/507,060
C--> 29 <141> CURRENT FILING DATE: 2004-09-09
  29 <150> PRIOR APPLICATION NUMBER: GB 0206215.6
  31 <151> PRIOR FILING DATE: 2002-03-15
  35 <160> NUMBER OF SEQ ID NOS: 4
  39 <170> SOFTWARE: PatentIn version 3.1
  43 <210> SEQ ID NO: 1
  45 <211> LENGTH: 15
  47 <212> TYPE: PRT
  49 <213> ORGANISM: Artificial sequence
  53 <220> FEATURE:
  55 <223> OTHER INFORMATION: LAT-11 is an artificial sequence for use in the ZAP-70 kinase
ass
  56         ay
  58 <220> FEATURE:
  60 <221> NAME/KEY: MISC_FEATURE
  62 <222> LOCATION: (1)..(1)
  64 <223> OTHER INFORMATION: X=L(+)-biotinyl-aminohexanoyl
  68 <400> SEQUENCE: 1
W--> 70 Xaa Glu Glu Gly Ala Pro Asp Tyr Glu Asn Leu Gln Gln Leu Asn
  71 1               5                   10                  15
  74 <210> SEQ ID NO: 2
  76 <211> LENGTH: 12
  78 <212> TYPE: PRT
  80 <213> ORGANISM: Artificial sequence
  84 <220> FEATURE:
  86 <223> OTHER INFORMATION: Biot-Y397 is a sequence for use in FAK assay
  88 <220> FEATURE:
  90 <221> NAME/KEY: MISC_FEATURE
```

[Handwritten annotations:]

see item 4 on Error Summary Sheet

Does Not Comply Corrected Diskette Needed

pp 1-2

give source of genetic material (see item 11 on Error Summary Sheet)

Xaa can only represent a single amino acid, nothing else. (see item 13 on Error Summary Sheet)

give source

RAW SEQUENCE LISTING   DATE: 09/23/2004
PATENT APPLICATION: US/10/507,060   TIME: 11:58:50

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\09232004\J507060.raw**

```
 92 <222> LOCATION: (1)..(1)
 94 <223> OTHER INFORMATION: Biotin        Xaa can only represent a single
 98 <400> SEQUENCE: 2                       amino acid
W--> 100 Xaa Ser Glu Thr Asp Asp Tyr Ala Glu Ile Ile Asp
101 1               5                   10
104 <210> SEQ ID NO: 3
106 <211> LENGTH: 21
108 <212> TYPE: DNA
110 <213> ORGANISM: Artificial sequence
114 <220> FEATURE:
116 <223> OTHER INFORMATION: PCR primer for preparing human FAK cDNA
118 <400> SEQUENCE: 3
119 atggcagctg cttaccttga c                                              21
122 <210> SEQ ID NO: 4
124 <211> LENGTH: 21
126 <212> TYPE: DNA
128 <213> ORGANISM: Artificial sequence
132 <220> FEATURE:
134 <223> OTHER INFORMATION: PCR primer for preparing human FAK cDNA
136 <400> SEQUENCE: 4
137 tcagtgtggt ctcgtctgcc c                                              21
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/23/2004
PATENT APPLICATION: US/10/507,060   TIME: 11:58:51

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\09232004\J507060.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1
Seq#:2; Xaa Pos. 1

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/507,060

DATE: 09/23/2004
TIME: 11:58:51

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\09232004\J507060.raw**

L:29 M:270 C: Current Application Number differs, Replaced Current Application No
L:29 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0